



Exhibit 1

- X - 82

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- T830X
- (i) APPLICANTS: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
- (ii) TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORGAN & FINNEGAN  
(B) STREET: 345 PARK AVENUE  
(C) CITY: NEW YORK  
(D) STATE: NEW YORK  
(E) COUNTRY: USA  
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: FLOPPY DISK  
(B) COMPUTER: IBM PC COMPATIBLE  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/231,565  
(B) FILING DATE: 22-APR-1994  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: CAROL M. GRUPPI  
(B) REGISTRATION NUMBER: 37,341  
(C) REFERENCE/DOCKET NUMBER: 2026-4124
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 758-4800  
(B) TELEFAX: (212) 751-6849  
(C) TELEX: 421792
- B'

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1559  
(B) TYPE: NUCLEOTIDE  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: UNKNOWN
- (ii) MOLECULE TYPE: cDNA
- 83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAGACAGA GGACTCTCAT TAAGGAAGGT GTCCTGTGCC 40  
CTGACCCTAC AAGATGCCAA GAGAAGATGC TCACTTCATC 80  
TATGGTTACC CCAAGAAGGG GCACGGCCAC TCTTACACCA 120  
CGGCTGAAGA GGCCGCTGGG ATCGGCATCC TGACAGTGAT 160  
CCTGGGAGTC TTACTGCTCA TCGGCTGTTG GTATTGTAGA 200  
AGACGAAATG GATACAGAGC CTTGATGGAT AAAAGTCTTC 240  
ATGTTGGCAC TCAATGTGCC TTAACAAGAA GATGCCCACA 280  
AGAAGGGTTT GATCATCGGG ACAGCAAAGT GTCTCTTCAA 320  
GAGAAAAACT GTGAACCTGT GGTTCCCAAT GCTCCACCTG 360  
CTTATGAGAA ACTCTCTGCA GAACAGTCAC CACCACCTTA 400  
TTCACCTTAA GAGCCAGCGA GACACCTGAG ACATGCTGAA 440  
ATTATTTCTC TCACACTTTT GCTTGAATTT AATACAGACA 480  
TCTAATGTTT TCCTTTGGAA TGGTGTAGGA AAAATGCAAG 520  
CCATCTCTAA TAATAAGTCA GTGTTAAAAT TTTAGTAGGT 560  
CCGCTAGCAG TACTAATCAT GTGAGGAAAT GATGAGAAAT 600  
ATTAAATTGG GAAAACTCCA TCAATAAATG TTGCAATGCA 640  
TGATACTATC TGTGCCAGAG GTAATGTTAG TAAATCCATG 680  
GTGTTATTTT CTGAGAGACA GAATTCAAGT GGGTATTCTG 720  
GGGCCATCCA ATTTCTCTTT ACTTGAAATT TGGCTAATAA 760  
CAAAC TAGTC AGGTTTTCGA ACCTTGACCG ACATGAACTG 800  
TACACAGAAT TGTTCCAGTA CTATGGAGTG CTCACAAAGG 840  
ATACTTTTAC AGGTTAAGAC AAAGGGTTGA CTGGCCTATT 880  
TATCTGATCA AGAACATGTC AGCAATGTCT CTTTGTGCTC 920  
TAAAATTCTA TTATACTACA ATAATATATT GTAAAGATCC 960

B'  
Cont.

84

- 2 - 84

B' Cmt.

TATAGCTCTT TTTTTTTGAG ATGGAGTTTC GCTTTTGTG	1000
CCCAGGCTGG AGTGCAATGG CGCGATCTTG GCTCACCATA	1040
ACCTCCGCCT CCCAGGTTCA AGCAATTCTC CTGCCTTAGC	1080
CTCCTGAGTA GCTGGGATTA CAGGCGTGCG CCACTATGCC	1120
TGACTAATTT TGTAGTTTTA GTAGAGACGG GGTTCCTCCA	1160
TGTTGGTCAG GCTGGTCTCA AACTCCTGAC CTCAGGTGAT	1200
CTGCCCCGCT CAGCCTCCCA AAGTGCTGGA ATTACAGGCG	1240
TGAGCCACCA CGCCTGGCTG GATCCTATAT CTTAGGTAAG	1280
ACATATAACG CAGTCTAATT ACATTTCACT TCAAGGCTCA	1320
ATGCTATTCT AACTAATGAC AAGTATTTTC TACTAAACCA	1360
GAAATTGGTA GAAGGATTTA AATAAGTAAA AGCTACTATG	1400
TACTGCCTTA GTGCTGATGC CTGTGTACTG CCTTAAATGT	1440
ACCTATGGCA ATTTAGCTCT CTTGGGTTCC CAAATCCCTC	1480
TCACAAGAAT GTGCAGAAGA AATCATAAAG GATCAGAGAT	1520
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1559

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Arg	Glu	Asp	Ala	His	Phe	Ile	Tyr	Gly	Tyr	Pro	Lys
1				5						10			
Lys	Gly	His	Gly	His	Ser	Tyr	Thr	Thr	Ala	Glu	Glu	Ala	Ala
15					20					25			

- A - 85

B<sup>1</sup>  
Cont.

Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu  
30 35 40

Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala  
45 50 55

Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu  
60 65 70

Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser  
75 80

Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro  
85 90 95

Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser  
100 105 110

Pro Pro Pro Tyr Ser Pro  
115

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Ala Glu Glu Ala Ala Gly Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Gly Ile Gly Ile Leu Thr Val  
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

B'  
cont.

Gly Ile Gly Ile Leu Thr Val Ile Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ile Leu Thr Val Ile Leu Gly Val  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

87

Ile Leu Thr Val Ile Leu Gly Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Val Ile Leu Gly Val Leu Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Ile Leu Gly Val Leu Leu Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

- 788 -

Val Ile Leu Gly Val Leu Leu Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

B1  
Cont.

Ala Leu Met Asp Lys Ser Leu His Val  
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu His Val Gly Thr Gln Cys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

89

- 8 - 89

Pro Val Val Pro Asn Ala Pro Pro Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Ala Pro Pro Ala Tyr Glu Lys Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:



90  
- 8 -

Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

B' Cnt-  
Glu Ala Ala Gly Ile Gly Ile Leu Thr Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Gly Ile Gly Ile Leu Thr Val Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

9/  
- 10 -

Gly Ile Leu Thr Val Ile Leu Gly Val Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Leu Thr Val Ile Leu Gly Val Leu Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Val Ile Leu Gly Val Leu Leu Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Val Ile Leu Gly Val Leu Leu Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

B' Cnt.  
Arg Ala Leu Met Asp Lys Ser Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Leu His Val Gly Thr Gln Cys Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Unknown
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gln Glu Lys Asn Cys Glu Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2172  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

B' Cont.

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680

B  
Cont.

TTCTCCGTGA	GCGTGTCCCA	GTTGCGGGCC	TTGGATGGAG	720
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACTT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCTC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAAGTGCAG	AGGCCCTTAA	1000
CACCACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120
TGCACCTGTG	CAGATGCCAA	CTGCAGAGAG	CACAGGTATG	1160
ACACCTGAGA	AGGTGCCAGT	TTCAGAGGTC	ATGGGTACCA	1200
CACTGGCAGA	GATGTCAACT	CCAGAGGCTA	CAGGTATGAC	1240
ACCTGCAGAG	GTATCAATTG	TGGTGCTTTC	TGGAACCACA	1280
GCTGCACAGG	TAACAACCTAC	AGAGTGGGTG	GAGACCACAG	1320
CTAGAGAGCT	ACCTATCCCT	GAGCCTGAAG	GTCCAGATGC	1360
CAGCTCAATC	ATGTCTACGG	AAAGTATTAC	AGGTTCCCTG	1400
GGCCCCCTGC	TGGATGGTAC	AGCCACCTTA	AGGCTGGTGA	1440
AGAGACAAGT	CCCCCTGGAT	TGTGTTCTGT	ATCGATATGG	1480
TTCCTTTTCC	GTCACCCTGG	ACATTGTCCA	GGGTATTGAA	1520
AGTGCCGAGA	TCCTGCAGGC	TGTGCCGTCC	GGTGAGGGGG	1560
ATGCATTTGA	GCTGACTGTG	TCCTGCCAAG	GCGGGCTGCC	1600
CAAGGAAGCC	TGCATGGAGA	TCTCATCGCC	AGGGTGCCAG	1640
CCCCCTGCCC	AGCGGCTGTG	CCAGCCTGTG	CTACCCAGCC	1680

B' cont.

CAGCCTGCCA GCTGGTCTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAATAAAAAA TAAAAATAAA AAAAAATAAA	2160
AAAAATAAAA AA	2172

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Asp	Leu	Val	Leu	Lys	Arg	Cys	Leu	Leu	His	Leu
1				5						10	

Ala Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr  
                   15                                  20  
 Lys Val Pro Arg Asn Gln Asp Trp Leu Gly Val Ser  
 25                                  30                                  35  
 Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu  
                                   40                                  45  
 Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys  
                   50                                  55                                  60  
 Trp Arg Gly Gly Gln Val Ser Leu Lys Val Ser Asn  
                                   65                                  70  
 Asp Gly Pro Thr Leu Ile Gly Ala Asn Ala Ser Phe  
                                   75                                  80  
 Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val  
 85                                  90                                  95  
 Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr  
                                   100                                  105  
 Ile Ile Asn Gly Ser Gln Val Trp Gly Gly Gln Pro  
                   110                                  115                                  120  
 Val Tyr Pro Gln Glu Thr Asp Asp Ala Cys Ile Phe  
                                   125                                  130  
 Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser  
                                   135                                  140  
 Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp  
 145                                  150                                  155  
 Gly Gln Tyr Trp Gln Phe Leu Gly Gly Pro Val Ser  
                                   160                                  165  
 Gly Leu Ser Ile Gly Thr Gly Arg Ala Met Leu Gly  
                   170                                  175                                  180  
 Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg  
                                   185                                  190  
 Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser  
                                   195                                  200  
 Ser Ala Phe Thr Ile Thr Asp Gln Val Pro Phe Ser  
 205                                  210                                  215  
 Val Ser Val Ser Gln Leu Arg Ala Leu Asp Gly Gly  
                                   220                                  225  
 Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe  
                   230                                  235                                  240  
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala  
                                   245                                  250  
 Glu Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp  
                                   255                                  260  
 Ser Ser Gly Thr Leu Ile Ser Arg Ala Leu Val Val  
 260                                  265                                  270  
 Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala  
                                   275                                  280  
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser  
                   285                                  290                                  295  
 Cys Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Gly  
                                   300                                  305  
 His Arg Pro Thr Ala Glu Ala Pro Asn Thr Thr Ala  
                   310                                  315

B'  
Cont.

97

Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Val	Gly	Thr	Thr
320					325					330	
Pro	Gly	Gln	Ala	Pro	Thr	Ala	Glu	Pro	Ser	Gly	Thr
			335					340			
Thr	Ser	Val	Gln	Val	Pro	Thr	Thr	Glu	Val	Ile	Ser
345						350				355	
Thr	Ala	Pro	Val	Gln	Met	Pro	Thr	Ala	Glu	Ser	Thr
				360					365		
Gly	Met	Thr	Pro	Glu	Lys	Val	Pro	Val	Ser	Glu	Val
		370					375				
Met	Gly	Thr	Thr	Leu	Ala	Glu	Met	Ser	Thr	Pro	Glu
380					385					390	
Ala	Thr	Gly	Met	Thr	Pro	Ala	Glu	Val	Ser	Ile	Val
			395					400			
Val	Leu	Ser	Gly	Thr	Thr	Ala	Ala	Gln	Val	Thr	Thr
405						410				415	
Thr	Glu	Trp	Val	Glu	Thr	Thr	Ala	Arg	Glu	Leu	Pro
				420					425		
Ile	Pro	Glu	Pro	Glu	Gly	Pro	Asp	Ala	Ser	Ser	Ile
		430					435				
Met	Ser	Thr	Glu	Ser	Ile	Thr	Gly	Ser	Leu	Gly	Pro
440					445					450	
Leu	Leu	Asp	Gly	Thr	Ala	Thr	Leu	Arg	Leu	Val	Lys
			455					460			
Arg	Gln	Val	Pro	Leu	Asp	Cys	Val	Leu	Tyr	Arg	Tyr
465						470				475	
Gly	Ser	Phe	Ser	Val	Thr	Leu	Asp	Ile	Val	Gln	Gly
				480					490		
Ile	Glu	Ser	Ala	Glu	Ile	Leu	Gln	Ala	Val	Pro	Ser
		495					500				
Gly	Glu	Gly	Asp	Ala	Phe	Glu	Leu	Thr	Val	Ser	Cys
505					510					515	
Gln	Gly	Gly	Leu	Pro	Lys	Glu	Ala	Cys	Met	Glu	Ile
			520					525			
Ser	Ser	Pro	Gly	Cys	Gln	Pro	Pro	Ala	Gln	Arg	Leu
530						535				540	
Cys	Gln	Pro	Val	Leu	Pro	Ser	Pro	Ala	Cys	Gln	Leu
				545					550		
Val	Leu	His	Gln	Ile	Leu	Lys	Gly	Gly	Ser	Gly	Thr
		555					560				
Tyr	Cys	Leu	Asn	Val	Ser	Leu	Ala	Asp	Thr	Asn	Ser
565					570					575	
Leu	Ala	Val	Val	Ser	Thr	Gln	Leu	Ile	Met	Pro	Gly
			580					585			
Gln	Glu	Ala	Gly	Leu	Gly	Gln	Val	Pro	Leu	Ile	Val
590						595				600	
Gly	Ile	Leu	Leu	Val	Leu	Met	Ala	Val	Val	Leu	Ala
				605					610		
Ser	Leu	Ile	Tyr	Arg	Arg	Arg	Leu	Met	Lys	Gln	Asp
		615					620				



98  
- 27 -

Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His  
625 630 635  
Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro  
640 645  
Ile Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln  
650 655 660  
Val

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Pro Gly Ile Leu Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Leu Ser Gly Gln Gln Val  
1 5

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Pro Pro Gln Trp Ala Ala Gly Leu Ser Thr Leu Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Leu Asp Gly Gly Asn Lys His Phe Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Leu Lys Arg Cys Leu Leu His Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Leu Pro Ser Pro Ala Cys Gln Leu Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Leu Ala Asp Thr Asn Ser Leu Ala Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Val Ser Val Ser Gln Leu Arg Ala  
1 5

B' cont.  
(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Tyr Leu Glu Pro Gly Pro Val Thr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Asn Val Ser Leu Ala Asp Thr Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58  
(B) TYPE: NUCLEOTIDE  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGACAGGCCG AGGCGGCCTT TTTTTTTTTT TTTTTTTTTT 40  
TTTTTTTTTT TTTTTTTT 58

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12  
(B) TYPE: NUCLEOTIDE  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAATCGCGA CC 12

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15  
(B) TYPE: NUCLEOTIDE  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTCGCGATT GGTA 15

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Ile Leu Gly Phe Val Phe Thr Leu  
1 5

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